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SEQUENCE LISTING

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CHEN, JUI-LIN
YANG, NING-SUN

<120> A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, 3-1,
4-BETA-D-GLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY AND
THERMO-TOLERANCE

<130> 4910-8

<140> 09/654,652

<141> 2000-09-05

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Modified enzyme
with enhanced activity and thermal stability

<400> 1

Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu
1 5 10 15

Glu Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala
20 25 30

Ser Gly Thr Val Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile
35 40 45

Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys
50 55 60

Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
65 70 75 80

Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln
85 90 95

Ala Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp
100 105 110

Thr Val Asp Gly Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser
115 120 125

Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu
130 135 140

Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
145 150 155 160

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Phe | Ile | Asn | Trp | Val | Lys | Val | Tyr | Lys | Tyr | Thr | Pro | Gly | Gln | Gly | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Glu | Gly | Gly | Ser | Asp | Phe | Thr | Leu | Asp | Trp | Thr | Asp | Asn | Phe | Asp | Thr | |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| Phe | Asp | Gly | Ser | Arg | Trp | Gly | Lys | Gly | Asp | Trp | Thr | Phe | Asp | Gly | Asn | |
| | | | | 195 | | | | | 200 | | | | | 205 | | |
| Arg | Val | Asp | Leu | Thr | Asp | Lys | Asn | Ile | Tyr | Ser | Arg | Asp | Gly | Met | Leu | |
| | | | | 210 | | | | | 215 | | | | | 220 | | |
| Ile | Leu | Ala | Leu | Thr | Arg | Lys | Gly | Gln | Glu | Ser | Phe | Asn | Gly | Gln | Val | |
| | | | | 225 | | | | | 230 | | | | | 235 | | |
| Pro | Arg | Asp | Asp | Glu | Pro | Ala | Pro | | | | | | | | | |
| | | | | 245 | | | | | | | | | | | | |

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<210> 2
<211> 267
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Modified enzyme
with enhanced activity and thermal stability

| | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> | 2 | | | | | | | | | | | | | | | |
| Met | Val | Ser | Ala | Lys | Asp | Phe | Ser | Gly | Ala | Glu | Leu | Tyr | Thr | Leu | Glu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Glu | Val | Gln | Tyr | Gly | Lys | Phe | Glu | Ala | Arg | Met | Lys | Met | Ala | Ala | Ala | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ser | Gly | Thr | Val | Ser | Ser | Met | Phe | Leu | Tyr | Gln | Asn | Gly | Ser | Glu | Ile | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ala | Asp | Gly | Arg | Pro | Trp | Val | Glu | Val | Asp | Ile | Glu | Val | Leu | Gly | Lys | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Asn | Pro | Gly | Ser | Phe | Gln | Ser | Asn | Ile | Ile | Thr | Gly | Lys | Ala | Gly | Ala | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Gln | Lys | Thr | Ser | Glu | Lys | His | His | Ala | Val | Ser | Pro | Ala | Ala | Asp | Gln | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Phe | His | Thr | Tyr | Gly | Leu | Glu | Trp | Thr | Pro | Asn | Tyr | Val | Arg | Trp | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Thr | Val | Asp | Gly | Gln | Glu | Val | Arg | Lys | Thr | Glu | Gly | Gly | Gln | Val | Ser | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Leu | Thr | Gly | Thr | Gln | Gly | Leu | Arg | Phe | Asn | Leu | Trp | Ser | Ser | Glu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |

Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
 145 150 155 160
 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly
 165 170 175
 Glu Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr
 180 185 190
 Phe Asp Gly Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn
 195 200 205
 Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu
 210 215 220
 Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
 225 230 235 240
 Pro Arg Asp Asp Glu Pro Ala Pro Asn Ser Ser Ser Val Asp Lys Leu
 245 250 255
 Ala Ala Ala Leu Glu His His His His His His
 260 265

<210> 3
 <211> 349
 <212> PRT
 <213> Fibrobacter succinogenes

<400> 3
 Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala
 1 5 10 15
 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly
 20 25 30
 Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr Gly Lys Phe Glu Ala
 35 40 45
 Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe Leu
 50 55 60
 Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
 65 70 75 80
 Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile
 85 90 95
 Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala
 100 105 110
 Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr Tyr Gly Leu Glu Trp
 115 120 125
 Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg Lys
 130 135 140

Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
145 150 155 160

Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp
165 170 175

Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr
180 185 190

Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser Asp Phe Thr Leu Asp
195 200 205

Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys Gly
210 215 220

Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
225 230 235 240

Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln
245 250 255

Glu Ser Phe Asn Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln
260 265 270

Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser
275 280 285

Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser Ser
290 295 300

Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
305 310 315 320

Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn
325 330 335

Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
340 345

<210> 4

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding a
modified enzyme

<220>

<221> CDS

<222> (1)..(744)

<400> 4

atg gtt agc gca aag gat ttt agc ggt gcc gaa ctc tac acg tta gaa
Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu
1 5 10 15

| | |
|---|-----|
| gaa gtt cag tac ggt aag ttt gaa gcc cgt atg aag atg gca gcc gca | 96 |
| Glu Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala | |
| 20 25 30 | |
| tcg gga aca gtc agt tcc atg ttc ctc tac cag aat ggt tcc gaa atc | 144 |
| Ser Gly Thr Val Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile | |
| 35 40 45 | |
| gcc gat gga agg ccc tgg gta gaa gtg gat att gaa gtt ctc ggc aag | 192 |
| Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys | |
| 50 55 60 | |
| aat ccg ggc agt ttc cag tcc aac atc att acc ggt aag gcc ggc gca | 240 |
| Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala | |
| 65 70 75 80 | |
| caa aag act agc gaa aag cac cat gct gtt agc ccc gcc gcc gat cag | 288 |
| Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln | |
| 85 90 95 | |
| gct ttc cac acc tac ggt ctc gaa tgg act ccg aat tac gtc cgc tgg | 336 |
| Ala Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp | |
| 100 105 110 | |
| act gtt gac ggt cag gaa gtc cgc aag acg gaa ggt ggc cag gtt tcc | 384 |
| Thr Val Asp Gly Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser | |
| 115 120 125 | |
| aac ttg aca ggt aca cag gga ctc cgt ttt aac ctt tgg tcg tct gag | 432 |
| Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu | |
| 130 135 140 | |
| agt gcg gct tgg gtt ggc cag ttc gat gaa tca aag ctt ccg ctt ttc | 480 |
| Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe | |
| 145 150 155 160 | |
| cag ttc atc aac tgg gtc aag gtt tat aag tat acg ccg ggc cag ggc | 528 |
| Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly | |
| 165 170 175 | |
| gaa ggc ggc agc gac ttt acg ctt gac tgg acc gac aat ttt gac acg | 576 |
| Glu Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr | |
| 180 185 190 | |
| ttt gat ggc tcc cgc tgg ggc aag ggt gac tgg aca ttt gac ggt aac | 624 |
| Phe Asp Gly Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn | |
| 195 200 205 | |
| cgt gtc gac ctc acc gac aag aac atc tac tcc aga gat ggc atg ttg | 672 |
| Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu | |
| 210 215 220 | |
| atc ctc gcc ctc acc cgc aaa ggt cag gaa agc ttc aac ggc cag gtt | 720 |
| Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val | |
| 225 230 235 240 | |

ccg aga gat gac gaa cct gct ccg
 Pro Arg Asp Asp Glu Pro Ala Pro
 245

744

<210> 5
 <211> 804
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DNA encoding a
 modified enzyme

<220>
 <221> CDS
 <222> (1)..(804)

<400> 5
 atg gtt agc gca aag gat ttt agc ggt gcc gaa ctc tac acg tta gaa 48
 Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu
 1 5 10 15
 gaa gtt cag tac ggt aag ttt gaa gcc cgt atg aag atg gca gcc gca 96
 Glu Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala
 20 25 30
 tcg gga aca gtc agt tcc atg ttc ctc tac cag aat ggt tcc gaa atc 144
 Ser Gly Thr Val Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile
 35 40 45
 gcc gat gga agg ccc tgg gta gaa gtg gat att gaa gtt ctc ggc aag 192
 Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys
 50 55 60
 aat ccg ggc agt ttc cag tcc aac atc att acc ggt aag gcc ggc gca 240
 Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
 65 70 75 80
 caa aag act agc gaa aag cac cat gct gtt agc ccc gcc gcc gat cag 288
 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln
 85 90 95
 gct ttc cac acc tac ggt ctc gaa tgg act ccg aat tac gtc cgc tgg 336
 Ala Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp
 100 105 110
 act gtt gac ggt cag gaa gtc cgc aag acg gaa ggt ggc cag gtt tcc 384
 Thr Val Asp Gly Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser
 115 120 125
 aac ttg aca ggt aca cag gga ctc cgt ttt aac ctt tgg tcg tct gag 432
 Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu
 130 135 140
 agt gcg gct tgg gtt ggc cag ttc gat gaa tca aag ctt ccg ctt ttc 480
 Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
 145 150 155 160

| | |
|---|-----|
| cag ttc atc aac tgg gtc aag gtt tat aag tat acg ccg ggc cag ggc | 528 |
| Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly | |
| 165 170 175 | |
| | |
| gaa ggc ggc agc gac ttt acg ctt gac tgg acc gac aat ttt gac acg | 576 |
| Glu Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr | |
| 180 185 190 | |
| | |
| ttt gat ggc tcc cgc tgg ggc aag ggt gac tgg aca ttt gac ggt aac | 624 |
| Phe Asp Gly Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn | |
| 195 200 205 | |
| | |
| cgt gtc gac ctc acc gac aag aac atc tac tcc aga gat ggc atg ttg | 672 |
| Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu | |
| 210 215 220 | |
| | |
| atc ctc gcc ctc acc cgc aaa ggt cag gaa agc ttc aac ggc cag gtt | 720 |
| Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val | |
| 225 230 235 240 | |
| | |
| ccg aga gat gac gaa cct gct ccg aat tcg agc tcc gtc gac aag ctt | 768 |
| Pro Arg Asp Asp Glu Pro Ala Pro Asn Ser Ser Ser Val Asp Lys Leu | |
| 245 250 255 | |
| | |
| gcg gcc gca ctc gag cac cac cac cac cac tga | 804 |
| Ala Ala Ala Leu Glu His His His His His His | |
| 260 265 | |

<210> 6
 <211> 1050
 <212> DNA
 <213> Fibrobacter succinogenes

<220>
 <221> CDS
 <222> (1)..(1047)

| | |
|---|-----|
| <400> 6 | |
| atg aac atc aag aaa act gca gtc aag agc gct ctc gcc gta gca gcc | 48 |
| Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala | |
| 1 5 10 15 | |
| | |
| gca gca gca gcc ctc acc acc aat gtt agc gca aag gat ttt agc ggt | 96 |
| Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly | |
| 20 25 30 | |
| | |
| gcc gaa ctc tac acg tta gaa gaa gtt cag tac ggt aag ttt gaa gcc | 144 |
| Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr Gly Lys Phe Glu Ala | |
| 35 40 45 | |
| | |
| cgt atg aag atg gca gcc gca tcg gga aca gtc agt tcc atg ttc ctc | 192 |
| Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe Leu | |
| 50 55 60 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tac | cag | aat | ggg | tcc | gaa | atc | gcc | gat | gga | agg | ccc | tgg | gta | gaa | gtg | 240 |
| Tyr | Gln | Asn | Gly | Ser | Glu | Ile | Ala | Asp | Gly | Arg | Pro | Trp | Val | Glu | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| gat | att | gaa | gtt | ctc | ggc | aag | aat | ccg | ggc | agt | ttc | cag | tcc | aac | atc | 288 |
| Asp | Ile | Glu | Val | Leu | Gly | Lys | Asn | Pro | Gly | Ser | Phe | Gln | Ser | Asn | Ile | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| att | acc | ggg | aag | gcc | ggc | gca | caa | aag | act | agc | gaa | aag | cac | cat | gct | 336 |
| Ile | Thr | Gly | Lys | Ala | Gly | Ala | Gln | Lys | Thr | Ser | Glu | Lys | His | His | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| gtt | agc | ccc | gcc | gcc | gat | cag | gct | ttc | cac | acc | tac | ggg | ctc | gaa | tgg | 384 |
| Val | Ser | Pro | Ala | Ala | Asp | Gln | Ala | Phe | His | Thr | Tyr | Gly | Leu | Glu | Trp | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| act | ccg | aat | tac | gtc | cgc | tgg | act | gtt | gac | ggg | cag | gaa | gtc | cgc | aag | 432 |
| Thr | Pro | Asn | Tyr | Val | Arg | Trp | Thr | Val | Asp | Gly | Gln | Glu | Val | Arg | Lys | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| acg | gaa | ggg | ggc | cag | gtt | tcc | aac | ttg | aca | ggg | aca | cag | gga | ctc | cgt | 480 |
| Thr | Glu | Gly | Gly | Gln | Val | Ser | Asn | Leu | Thr | Gly | Thr | Gln | Gly | Leu | Arg | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| ttt | aac | ctt | tgg | tgc | tct | gag | agt | gcg | gct | tgg | gtt | ggc | cag | ttc | gat | 528 |
| Phe | Asn | Leu | Trp | Ser | Ser | Glu | Ser | Ala | Ala | Trp | Val | Gly | Gln | Phe | Asp | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| gaa | tca | aag | ctt | ccg | ctt | ttc | cag | ttc | atc | aac | tgg | gtc | aag | gtt | tat | 576 |
| Glu | Ser | Lys | Leu | Pro | Leu | Phe | Gln | Phe | Ile | Asn | Trp | Val | Lys | Val | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| aag | tat | acg | ccg | ggc | cag | ggc | gaa | ggc | ggc | agc | gac | ttt | acg | ctt | gac | 624 |
| Lys | Tyr | Thr | Pro | Gly | Gln | Gly | Glu | Gly | Gly | Ser | Asp | Phe | Thr | Leu | Asp | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| tgg | acc | gac | aat | ttt | gac | acg | ttt | gat | ggc | tcc | cgc | tgg | ggc | aag | ggg | 672 |
| Trp | Thr | Asp | Asn | Phe | Asp | Thr | Phe | Asp | Gly | Ser | Arg | Trp | Gly | Lys | Gly | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| gac | tgg | aca | ttt | gac | ggg | aac | cgt | gtc | gac | ctc | acc | gac | aag | aac | atc | 720 |
| Asp | Trp | Thr | Phe | Asp | Gly | Asn | Arg | Val | Asp | Leu | Thr | Asp | Lys | Asn | Ile | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| tac | tcc | aga | gat | ggc | atg | ttg | atc | ctc | gcc | ctc | acc | cgc | aaa | ggg | cag | 768 |
| Tyr | Ser | Arg | Asp | Gly | Met | Leu | Ile | Leu | Ala | Leu | Thr | Arg | Lys | Gly | Gln | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| gaa | agc | ttc | aac | ggc | cag | gtt | ccg | aga | gat | gac | gaa | cct | gct | ccg | caa | 816 |
| Glu | Ser | Phe | Asn | Gly | Gln | Val | Pro | Arg | Asp | Asp | Glu | Pro | Ala | Pro | Gln | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| tct | tct | agc | agc | gct | ccg | gca | tct | tct | agc | agt | gtt | ccg | gca | agc | tcc | 864 |
| Ser | Ser | Ser | Ser | Ala | Pro | Ala | Ser | Ser | Ser | Ser | Val | Pro | Ala | Ser | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |

| | |
|---|-----|
| tct agc gtc cct gcc tcc tcg agc agc gca ttt gtt ccg ccg agc tcc | 912 |
| Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser Ser | |
| 290 295 300 | |

| | |
|---|-----|
| tcg agc gcc aca aac gca atc cac gga atg cgc aca act ccg gca gtt | 960 |
| Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val | |
| 305 310 315 320 | |

| | |
|---|------|
| gca aag gaa cac cgc aat ctc gtg aac gcc aag ggt gcc aag gtg aac | 1008 |
| Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn | |
| 325 330 335 | |

| | |
|---|------|
| ccg aat ggc cac aag cgt tat cgc gtg aac ttt gaa cac taa | 1050 |
| Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His | |
| 340 345 | |

<210> 7
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

| | |
|-------------------------|----|
| <400> 7 | |
| tcaccacat ggtagcgca aag | 23 |

<210> 8
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

| | |
|-----------------------------|----|
| <400> 8 | |
| gccacgaatt ctgttcaaag ttcac | 25 |

<210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

| | |
|-------------------------------|----|
| <400> 9 | |
| cagccggcga tggccatggt tagcgca | 27 |

<210> 10
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

ctgctagaag aattcggagc aggttcgtc

29

<210> 11

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
illustrative peptide

<220>

<221> MOD_RES

<222> (2)

<223> An uncharged residue, such as Alanine, Proline or
Glutamine

<400> 11

Pro Xaa Ser Ser Ser Ser

1

5